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Explainable Artificial Intelligence in Multimodal Malaria Prediction: A Systematic Review and Roadmap Integrating Climate Change, Parasite Genomics, and Public Health Decision Support

Nalenhle Ndlovu [1]*, Belinda Ndlovu [2]**
[1,2]Informatics Department, National University of Science and Technology, Bulawayo, Zimbabwe
n02221862r@students.nust.ac.zw [1], belinda.ndlovu@nust.ac.zw [2]

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ABSTRACT

Malaria remains a persistent global public health burden, particularly in sub-Saharan Africa, requiring predictive systems that are both accurate and clinically interpretable. Although artificial intelligence (AI) has significantly improved malaria forecasting and diagnosis, real-world deployment remains constrained by opaque “black-box” decision pathways and fragmented modelling approaches that analyse climatic, genomic, and clinical drivers in isolation. This systematic review synthesises contemporary evidence on Explainable Artificial Intelligence (XAI) applications in malaria prediction, integrating climate vulnerability and parasite genomic insights. The review was conducted and reported in accordance with PRISMA 2009 guidelines. Four databases (PubMed, IEEE Xplore, SpringerLink, and ScienceDirect) were systematically searched, yielding 161 records; 12 studies published between 2020 and 2025 met the inclusion criteria. The restricted timeline reflects the recent surge in model-agnostic interpretability methods such as SHAP and LIME. Findings indicate that ensemble learning models, particularly Random Forest and XGBoost, demonstrate robust predictive performance and strong post hoc interpretability in climate-driven and clinical forecasting contexts. In contrast, deep learning architectures, including Convolutional Neural Networks and Transformers, excel in image-based and genomic classification tasks but require interpretability overlays to mitigate opacity. Despite methodological advances, Causal AI remains underutilised, limiting current models' capacity to simulate intervention scenarios and inform policy decision-making. Furthermore, no fully unified multimodal framework that integrates climatic, genomic, and clinical features into a single explainable architecture was identified. This review not only synthesises trends in algorithmic performance and interpretability but also establishes a strategic roadmap for developing unified, policy-integrated multimodal XAI systems that support transparent malaria risk prediction amid accelerating climate change and parasite evolutionary dynamics.

I. INTRODUCTION

Malaria is a mosquito-borne disease caused by protozoan parasites of the genus Plasmodium. [1]. The Anopheles mosquito thrives in warm and humid conditions, presenting a range of health-related issues such as elevated body temperature, headaches, nausea, vomiting, and diarrhoea [2], [3]. In severe cases, malaria can cause jaundice, seizures, coma, or even death [4]. Malaria remains a major public health challenge in developing nations, particularly in sub-Saharan Africa, with profound economic implications [5]. The disease represents a significant global health issue in the tropical regions of the world due to the prevailing climatic, ecological, and socio-economic factors that favour the persistence of the disease in these regions [6]. In the year 2022 alone, the number of cases of the disease exceeded 251 million in the African regions of the world, with the paediatric population of the region being the hardest hit due to the disease. [7], [8]. Pregnant women in the region are also being adversely affected due to the disease, as the disease causes significant negative impacts on the health of the individuals in the region[7]. Despite the significant improvements in the chemopreventive and control strategies of the disease in recent years, the disease still represents a significant challenge in the context of its eradication due to the complex relationship between the environmental factors and the evolution of the disease in the region [9]. Most of the reviews in the literature, such as in [10], [11], [12], focus primarily on the clinical diagnosis of the disease or the geospatial models of the disease in the region in an isolated manner; the importance of the interpretability of the models in the context of the integration of the genomics and climatic factors in the models has not received adequate attention in the literature as the models are not validated in the real world in the context of the evolution of the disease.

However, with the advancement in technologies such as Artificial Intelligence (AI) and Machine Learning (ML) in the health and malaria fields, transformative solutions and fresh insights have been achieved in health delivery systems [13],[14]. It is due to these technologies that it is now possible to process vast amounts of complex data and make accurate predictions regarding health and disease [15]–[17]. This is demonstrated in studies that have successfully implemented predictive modelling techniques to accurately evaluate and address hospital readmission threats in diabetic patients and develop personalized interventions for patients suffering from chronic health conditions [18],[19]. Such algorithms have successfully demonstrated their efficacy in addressing and managing different health conditions and threats, starting from chronic health conditions like diabetic patients to newly evolving health threats like infectious diseases [20]–[22]. Ensemble learning algorithms like Random Forest and eXtreme Gradient Boosting have demonstrated their efficacy in healthcare applications involving structured clinical and environmental health data [16],[23],[24]. While deep learning algorithms have demonstrated their efficacy in applications like image-based diagnoses and long-term climate-based forecasting [15],[25], [26]. It is also important to note that despite all these developments and their demonstrated efficacy in addressing different health and disease conditions and threats, existing studies have only demonstrated efficacy based on individual forms of health and clinical data and have failed to effectively integrate and represent different forms of malaria transmission threats [25], [27].

XAI has been identified as an important part of epidemiological models in dealing with the “black box” problem faced in ML models [6],[16],[28]. Having the “black box” in hand and being a major hurdle in the successful application of ML models in epidemiological studies, SHAP (SHapley Additive ExPlanations) and LIME (Local Interpretable Model-agnostic Explanations) have been used to make the ML models transparent and interpretable by “looking” into the inner workings of a “black box” system and “showing” the mechanisms behind the decisions being taken [26], [29], [30]. Recently, studies in neurological and ophthalmic diagnostics have been successful in using the tools of XAI in identifying the key biomarkers in the diseases, while gaining the trust of the medical professionals [31], [32]. Causal AI (CAI) has been a step forward in the improvement of the interpretability of ML models by “moving” from mere correlation to understanding the “why” behind the phenomena in the real world, by “focusing” on the cause-and-effect relationships in the real world [10]. The use of XAI tools is inconsistent in malaria studies, while the application of interpretability tools in the context of “multimodal” frameworks has not been explored in studies to date.

Despite significant advances in AI-based malaria prediction, studies remain limited and fragmented across climatic prediction, genomic research, and clinical diagnosis [3], [15], [33]. There has been a lack of research on the explainability of results across the three fields. While current studies are limited to genomic or environmental data, other disease prediction frameworks have begun to incorporate additional information streams, such as sentiment analysis of social media content, to predict infectious diseases [34]. Projected climate change scenarios and vector habitat expansion further amplify the need for adaptive, interpretable prediction systems.

Therefore, this review not only synthesizes algorithmic and interpretability approaches but also establishes a conceptual blueprint for a multimodal XAI framework that can guide a deployable malaria-prediction system and critically compares ensemble and deep learning models with respect to accuracy, transparency, and interpretability trade-offs. Unlike previous reviews that focused independently on either clinical diagnosis, climate vulnerability, or genomic analysis, and did not evaluate explainability requirements across these modalities. This study proposes a unified framework that enables transparent, interpretable, and policy-driven malaria predictions by combining climatic vulnerabilities and genomic insights, with interpretable modelling outputs. Hence, lay a foundation for clinically trustworthy, multi-domain predictive systems for malaria control.

The research is directed and guided by these four research questions:

1. How does the comparative prediction capability of integrated multi-modal models compare with that of single modality approaches in the context of malaria incidence prediction?
2. What are the ways in which the methods of "Explainable Artificial Intelligence" shed light on the role played by the combined data features in the outputs of complex malaria prediction models, and what influence does this have on the trust of stakeholders?
3. What is the performance of various algorithms of artificial intelligence and machine learning, in terms of their accuracy and applicability on various data modalities?
4. What actionable public health insights are available from XAI feature importance and causal inference to guide targeted malaria control interventions?

The rest of the paper is organized as follows. In Section II, the research methodology is presented. In Section III, the research results and the research gaps identified in the existing body of knowledge are discussed. In Section IV, the review concludes and outlines future research directions.

II. METHODS

The study utilized the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) standards in the process of conducting the study through the implementation of the four stages proposed in the protocol, namely the identification, screening, eligibility, and inclusion stages [35]. This study maintains the highest level of rigor in the study process, similar to what has been done in other systematic reviews [8], [31]. The complete search string for each database is provided in Appendix A. Inclusion and exclusion criteria were predefined prior to screening. A risk-of-bias assessment was conducted using a structured five-domain appraisal tool and visualized in ROBVIS.

A. Search Strategy

The search strategy employed Boolean and single-line searches to cover the concepts of Explainable AI (XAI), malaria prediction, climate, and genomic data, using multiple databases. The databases employed were PubMed, IEEE Xplore, SpringerLink, and ScienceDirect. The search commenced on the 19th of October 2025.

The search logic was employed as follows: *(“Explainable Artificial Intelligence” OR XAI OR “model interpretability”) AND (“SHAP” OR “LIME” OR “Random Forest” OR “XGBOOST”) AND (“malaria prediction” OR “malaria risk” OR “plasmodium forecasting”) AND (“climate data” OR “environmental variable” OR “meteorological data”) AND (“genomic data” OR “genetic sequence” OR “parasite genome”).*

The search retrieved 161 articles, including 48 from PubMed, 51 from Springer Nature, 29 from IEEE Xplore, and 33 from ScienceDirect.

B. Screening

During the screening process, 161 articles were selected from all databases and imported into Mendeley; 23 duplicates were removed, leaving 138 papers. After removing the duplicate papers, the total number of papers at this stage, together with the title and abstract, was screened and assessed based on the following criteria: use of AI or ML, relevance to malaria prediction, inclusion of genomic information or climate information, XAI frameworks that foster model interpretability, etc., 47 papers were removed at this stage.

While ensuring methodological rigor and systematicity, the procedure was undertaken prior to screening, in accordance with predetermined inclusion and exclusion criteria. Inclusion criteria were defined as studies published between 2020 and 2025. This was done to focus on the increased interest in explainable XAI models, driven by the adoption of SHAP and LIME in epidemiological models from 2020 onward.

C. Inclusion and exclusion criteria

These criteria have been developed through a highly selective process to ensure the appropriateness and quality of the information presented in the evidence. For the purposes of this systematic review, studies had to be empirical research papers published in conference proceedings or journals between 2020 and 2025. Studies on the application of AI/ML for predicting, diagnosing, or forecasting malaria infections are the primary focus of the literature reviewed in this paper. Additionally, the studies had to incorporate the concept of “explanation” or “model interpretability,” such as SHAP, LIME, or other feature-attribution methods, in the context of clinical decision-making. The inclusion of only 12 studies reflects the emerging, highly specific intersection among XAI, malaria prediction, climate vulnerability, and genomic integration. The low number suggests that fully integrated explainable multimodal malaria modelling remains an underdeveloped research frontier rather than a consequence of overly restrictive criteria. Finally, the studies had to be published in English.

To guide a search focused on actionable and evidence-based data, a filter to exclude literature from other databases can be implemented. Theoretical papers and opinion-type literature were excluded from consideration, as they did not provide empirical results for synthesis. Literature focused on clinical image diagnosis was excluded if it did not mention interpretability, to ensure that this literature was considered in this review and to address the “black box” issue in malaria prediction models. Literature without an accessible full text to assess quality was excluded from consideration.

D. Eligibility Criteria

The remaining 81 articles underwent assessment against all eligibility criteria. Emphasis was placed on the mandatory predefined inclusion and exclusion criteria to determine if they should be included in the systematic review. 43 articles were excluded, 38 were considered legible because they employed an empirical approach using XAI frameworks and reported relevant performance metrics.

E. Included

After the eligibility criteria were applied, the remaining 38 articles advanced to full-text review and met the inclusion criteria. After a thorough assessment, 26 studies were excluded because they focused on malaria but were not interpretable, did not use XAI models, or did not address core areas of the research questions. 12 papers were included for qualitative synthesis and data extraction.

F. Quality Assessment

The quality and risk of bias of the 12 included studies were critically appraised using a customized tool, a ROBVIS (Risk of Bias Visualization and Summary) framework. ROBVIS is a web application designed to visualise risk-of-bias assessments performed as part of a systematic review [21]. The evaluation focused on five key domains: (1) data quality and representativeness, (2) model development and validation, (3) explainability method implementation, (4) performance reporting, and (5) clinical/public health relevance. The overall assessment revealed a mixed risk of bias. While most studies demonstrated low risk in performance reporting and model development, concerns were frequently noted regarding data representativeness and the depth of implementation of explainability methods. This quality assessment informs the interpretation of the synthesis, suggesting that findings on feature importance and model generalizability should be interpreted with caution when the underlying data or XAI methods are limited.

The complete results of the bias assessment:


Risk of bias domains

Study	D1	D2	D3	D4	D5	Overall
Study 1	+	+	+	+	+	+
Study 2	+	-	+	+	+	+
Study 3	+	+	+	+	+	+
Study 4	X	+	+	-	-	X
Study 5	X	-	+	+	+	X
Study 6	+	-	X	+	+	-
Study 7	+	+	+	+	+	+
Study 8	-	-	+	+	+	+
Study 9	+	+	X	+	+	+
Study 10	-	+	X	+	+	-
Study 11	-	+	X	+	-	-
Study 12	X	+	X	+	+	-

Domains:
D1: Bias arising from the randomization process.
D2: Bias due to deviations from intended intervention.
D3: Bias due to missing outcome data.
D4: Bias in measurement of the outcome.
D5: Bias in selection of the reported result.

Judgement
X High
- Some concerns
+ Low

Figure 1. ROBVIS output

The identified risk-of-bias patterns informed the synthesis by weighting conclusions toward studies demonstrating robust validation, representative data, and substantive explainability, while treating findings from higher-risk studies as indicative rather than definitive in the output.

III. RESULTS AND DISCUSSIONS

This section presents the synthesized findings from 12 included studies through a comprehensive visual analysis of the PRISMA flow chart.

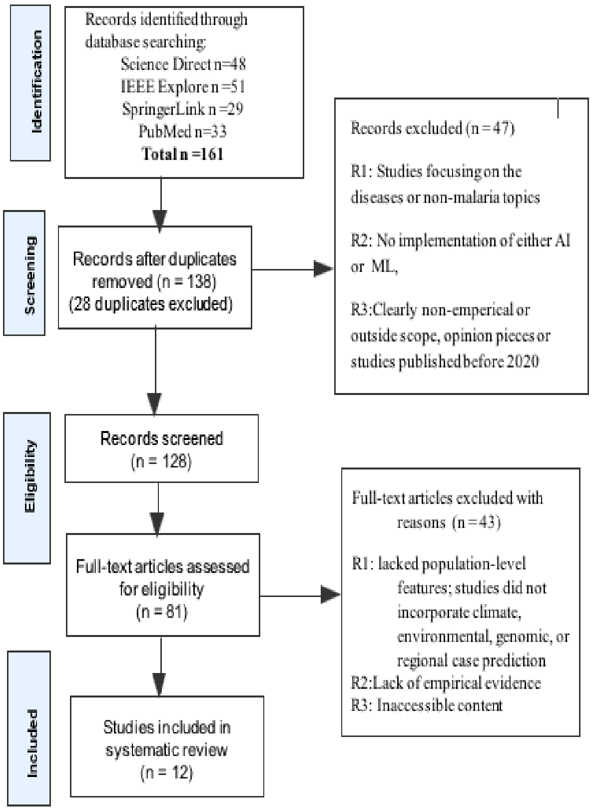

Figure 2. PRISMA screening results

TABLE 1
RESULTS TABLE

Author (Year)	**Title**	**Country**	**Data Modalities**	**Key Predictors**	**XAI Technique Applied**	**ML Algorithm Used**	**Reported Performance Metrics**	**i Challenges or Limitations**	**Key Findings**
[17]	Enhancing Malaria Incidence Prediction Using Weather Variables.	Rwanda	▪ Climatic ▪ Spatio-temporal (Daily incidence)	▪ Temperature ▪ Humidity ▪ Rainfall	Not mentioned (Focus on predictive power)	▪ Gradient Boosting Regression (GBR) ▪ Random Forest Regression (RFR)	GBR: R-squared 98.20%; RFR: R-squared 97.81% RMSE 671.52	Exceptionally high rate suggests a high risk of overfitting or data leakage in the time-series cross-validation.	Incorporating weather variables significantly enhances predictive performance. GBR slightly outperformed RFR.
[26]	Enhanced Malaria Detection Using Convolutional Neural Networks with SHAP and LIME for Model Interpretability	Algeria	▪ Blood smear images	▪ Image features (automatically extracted)	▪ SHAP ▪ LIME	▪ Convolutional Neural Networks (CNNs)	Mentions high effectiveness, specific metric not in abstract	Lack of interpretability in AI models limits widespread adoption. Limited to image data modality; CNNs are generally resource-intensive and require vast training data.	CNNs are effective for detection; XAI (SHAP, LIME) is essential for image-based deep learning models to address the black-box problem and establish trust by visualizing parasite-specific features.
[6]	Interpretable Machine Learning Models for Predicting Malaria	Uganda	▪ Clinical/Symptomatic Data ▪	▪ Clinical eneral (e.g., high fever, low platelet count, symptoms)	▪ SHAP ▪ LIME ▪	▪ XGBoost ▪ K-means ▪ KNN ▪ SVM ▪ Decision Tree ▪ Logistic Regression	Not explicitly detailed in the abstract	Lack of high-quality healthcare services and accurate diagnosis systems in underdeveloped regions. Focus is specifically on predicting *severe* malaria, not general case prediction or environmental factors.	Demonstrated a transparent approach to severe malaria prediction using XAI for meaningful interpretations.
[16]	An Explainable Artificial Intelligence Models for Predicting Malaria Risk in Kenya	Kenya	▪ Clinical Symptoms ▪ Environmental Factor ▪ Plasmodium Species	▪ Rainfall ▪ Temperature ▪ clinical symptoms	▪ SHAP ▪ Feature Importance ▪	▪ Random Forest ▪ Extreme Gradient Boosting (XGBoost)	Random Forest: 98% accuracy	Used synthetic data and over-sampling to address class imbalance. Reliance on a small synthetic dataset (N=1000) limits generalizability to real-world deployment.	Random Forest outperformed XGBoost. Critical predictors included clinical symptoms and environmental factors. SHAP identifies the combined clinical and environmental features as critical, promoting local trust.
[27]	Explainable AI for enhanced accuracy in malaria diagnosis using ensemble machine learning models	Nigeria	▪ Patient information (Clinical/Demographic data from 337 patients)	▪ clinical/demographic data from patient records	▪ LIME ▪ SHAP ▪ Permutation Feature Importance	▪ Random Forest ▪ AdaBoost ▪ Gradient Boost ▪ XGBoost, CatBoost	Mentions enhanced accuracy, specific metric not in abstract	Data gathered from a single medical centre (Federal Polytechnic Ilaro). Small, region-specific real-world dataset (N=337) limits broader generalizability and external validation.	Proposes the use of ensemble models with XAI for highly accurate and interpretable malaria diagnosis. Identify key diagnostic clinical markers in a resource-constrained, real-world setting.
[23]	Integrating machine learning and spatial clustering for malaria case prediction in Brazil's Legal Amazon	Brazil (Legal Amazon)	▪ Time-series ▪ Spatial Clustering Data ▪ Socioeconomic	▪ Primarily time-series data ▪ spatial cluster ID ▪ Geographic clustering ▪ .	▪ Not explicitly mentioned in the abstract.	▪ Random Forest (RF) ▪ LSTM ▪ GRU ▪ SVR ▪ XGBoost, ARIMA	Lowest RMSE (e.g., 0.00203) and MAE (RF outperformed others).	Traditional control measures have shown limited effectiveness, emphasizing the need for better predictive models. Performance is highly dependent on the initial spatial clustering methodology applied to segment the region.	Random Forest is the most robust and reliable model for short-term malaria case forecasting in the region. RF consistently outperforms complex deep learning (LSTM/GRU) and traditional time-series (ARIMA) models for

									clustered spatio-temporal forecasting.
[36])	Projecting malaria elimination in Thailand using Bayesian hierarchical spatiotemporal models	Thailand (provincial level)	▪ Malaria surveillance database (falciparum and vivax incidence) ▪ Spatiotemporal data ▪	▪ Space-time dynamic ▪ Species type (P. falciparum vs P. vivax)	▪ Model selection metrics (AIC/DIC)	▪ Bayesian hierarchical spatiotemporal models	Model Selection Metrics (DIC, WAIC)	Different predicted estimates between $P. falciparum$ and $P. vivax$ (difficulty in uniform elimination). Not a traditional ML/XAI study; it relies on strong prior statistical assumptions for modelling.	Provides crucial uncertainty intervals for projections, suggesting *P. falciparum* elimination is possible by 2024, guiding national policy.
[10]	Unraveling global malaria incidence and mortality using machine learning and artificial intelligence-driven spatial analysis	Global (106 countries)	▪ Epidemiological ▪ Socioeconomic ▪ Spatio-temporal (2000-2022)	▪ Socioeconomic factors ▪ geographical variables	▪ XAI (eXplainable AI) ▪ Causal AI (CAI)	▪ XGBoost (combined with XAI/CAI).	Employs rigorous spatial autocorrelation analyses (Getis-Ord Gi^* and Moran’s I).	Complexity of analysing heterogeneous, multi-source data from 106 countries. Large-scale analysis may mask critical local variability and heterogeneity in control measures.	Confirms the location of global high-risk areas (e.g., Nigeria, DRC) and provides causal relationships using CAI. Integration of XAI/CAI moves beyond correlation to establish key causal determinants of global malaria outcomes, enabling targeted policy.
[25]	Utilizing a novel high-resolution malaria dataset for climate-informed predictions with a deep learning transformer model	Southern Africa (Implied by context, focused on a novel regional dataset).	▪ Climatic ▪ Spatio-temporal (Daily incidence for 23 yrs) ▪ Climatic variables.	▪ Climatic factors ▪	▪ Novel Loss Function (Accounting for variability) ▪	▪ Deep Learning Transformer Model ▪ XGBoost, Statistical Model.	Transformer achieved AUROC of 80% (20–40% higher than comparative models).	Lack of applied deep learning studies for malaria in Southern Africa which leverage quality datasets. Requires advanced deep learning infrastructure and complex data processing pipelines.	The Transformer deep learning model, particularly with a novel loss function, significantly improves climate-informed malaria prediction accuracy.
[12]	Specialist hybrid models with asymmetric training for malaria prevalence prediction	Not specified in snippet.	▪ Malaria Prevalence Data.	Not specified	Not mentioned	Specialist hybrid models (likely involving time-series and neural networks/boosting).	Not detailed	Not detailed	Hybrid models are effective for malaria prevalence prediction.
[15]	Geographical classification of malaria parasites through applying machine learning to whole genome sequence data	Global (Genomic data from 27 countries for *P. falciparum* and 13 for *P. vivax*)	▪ Genomic Data (Whole Genome Sequencing /WGS, SNPs).	▪ Genomic factors (High-quality genome-wide SNPs).	Not explicitly mentioned in the abstract.	Deep Learning Convolutional Neural Network (CNN).	Classification methods had the lowest prediction error compared to regression models.	Uneven geographical sampling of isolates across the world; complexity of *Plasmodium* genetic diversity. Focused only on genomic data, it does not offer insights into climatic or clinical integration.	Deep learning on WGS data can accurately predict the geographical origin (down to the country-level) of *Plasmodium* infections.
[24]	Comparative analysis of machine learning models for malaria detection using validated synthetic data: a cost-sensitive approach with clinical domain knowledge integration	Sub-Saharan Africa (Synthetic)	▪ Clinical/Epidemiological features (Synthetic Dataset).	▪ Clinical and epidemiological features (synthetic data).	▪ Not explicitly mentioned in the abstract.	▪ XGBoost ▪ Naive Bayes ▪ Logistic Regression ▪ Random Forest ▪ Enhanced Bayesian Logistic Regression.	XGBoost achieved optimal AUC (0.956) and competitive clinical cost (5,496).	Relies on a synthetic dataset; generalizability needs confirmation with raw clinical data. Despite validation, it impacts direct clinical applicability assurance.	XGBoost provides the optimal balance between diagnostic performance and minimizing clinical cost when applied to detection.

According to Table 1, a comparative analysis indicates that ensemble models (RF, XGBoost) consistently demonstrate strong performance across structured clinical and climatic datasets with AUROC often exceeding 0.9. Deep learning models show superior performance in image and genomic classification but require interpretability overlays. However, performance metrics are reported inconsistently (e.g., AUROC, R², RMSE), limiting cross-study comparability. No study standardized evaluation across modality.

A. *Study Origin*

Figure 3 presents a continental map of research origins, highlighting the concentration of studies in malaria-endemic regions.

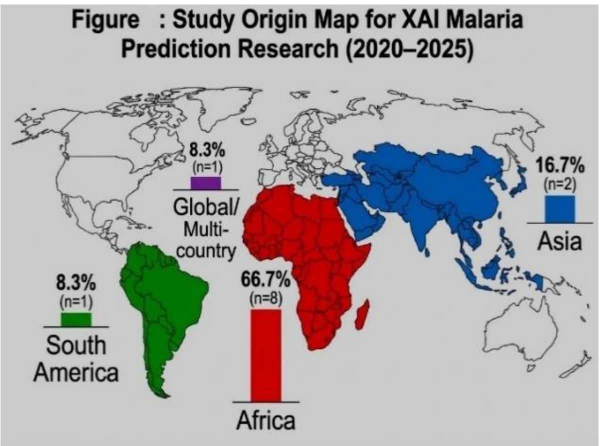

Figure 1. Study origin

Figure 3 reveals a pronounced geographical concentration in malaria-endemic regions, with Africa accounting for 66.7% (n = 8) of all included studies. Asia accounts for 16.7% (n=2), South America contributes 8.3% (n=1), and multi-country studies account for 8.3%, covering 106 countries for epidemiological analysis and 27-40 countries for genomic classification. This distribution highlights that research is appropriately concentrated in high-burden regions, such as sub-Saharan Africa. Although the volume of African studies is high, the extent of regional climatic heterogeneity remains underinvestigated. For example, rainfall-based malaria transmission in equatorial Africa, as observed in Rwanda, differs significantly from the semi-arid seasonal transmission observed in Southern Africa. In addition, the genomic variability of P. falciparum observed in West Africa differs significantly from that observed in Southeast Asia. However, none of the studies reviewed compared the interactions between climate and genomics across ecological zones. The future multimodal framework will include interactions among ecological zones and regional climate regimes.

B. *Description of the Evidence Synthesis*

Table 2 provides a structured summary of the key findings, gaps, and translational implications identified across the systematic literature review on AI applications for malaria prediction between 2020 and 2025.

TABLE 2
DESCRIPTION OF THE EVIDENCE SYNTHESIS

Clinical diagnostic AI	High-performance ML algorithms (XGBoost, Random Forest, CNN) accurately predict malaria diagnosis and severity using clinical symptoms or blood smear images.	XAI application remains siloed to clinical features, lacking the integration of external factors (climate vulnerability or parasite genomics) to provide contextualized diagnosis.	Provides rapid, objective diagnostic support to clinicians in low-resource settings, improving triage and treatment accuracy.	[6], [26], [37]
Explainability Techniques	SHAP and LIME are the dominant XAI techniques, used to interpret feature contributions in black-box models (XGBoost, CNN, RF). Causal AI is an emerging technique to move beyond correlation to establish causal links.	There is an inconsistent and fragmented use of XAI across modalities; virtually no study implements interpretability for a truly multi-modal framework unifying all three data types simultaneously.	Fosters trust and transparency among clinicians and administrators by providing attributable feature contributions for prediction outcomes.	[10], [26], [27]
Model validation and data Diversity	Models utilize robust validation techniques (cross-validation, bootstrap Cis) and comprehensive metrics (AUROC, RMSE). Use of validated synthetic data is noted to address scarcity	Lack of large-scale, standardized, and publicly available multi-modal datasets that unify clinical, genomic, and high-resolution environmental data.	Ensures the reliability and generalizability of predictive models, making them applicable across diverse epidemiological conditions and geographical regions.	[17], [24], [25]

As indicated in Table 2, ensemble techniques, including RF and XGB, demonstrate consistent, robust performance for both clinical and climate-based malaria prediction. These techniques also provide post hoc interpretability through SHAP and LIME. DL techniques are also seen to excel in image-based and genomic classification tasks. However, the black-box problem with DL techniques necessitates additional methods for explainability. Despite improvements in predictive accuracy, most studies continue to use single-modality data, which is analysed in isolation.

These findings have important implications for the use of the techniques for real-world applications. Although the use of XAI techniques improves interpretability, the findings also indicate variability in their application. The use of multiple data modalities remains fragmented. In conclusion, the findings of the studies indicate the importance of developing a unified framework for the use of multimodal data that demonstrates strong predictive performance and interpretability.

C. Frequency of Algorithms (2020-2025)

Figure 4 shows how Random Forest and XGBoost dominate across most data modalities, while SHAP and LIME are the most applied interpretability tools, especially for ensemble architectures and image-based models

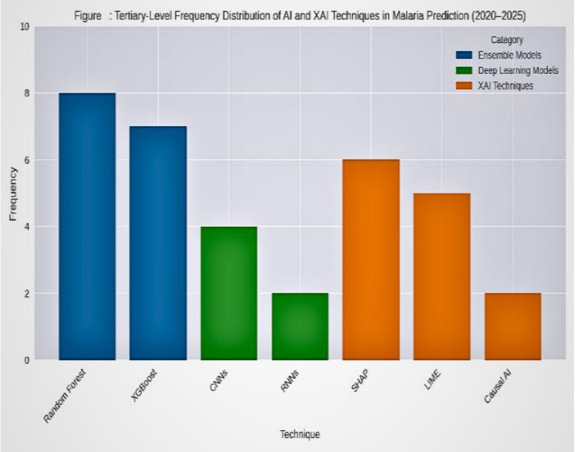

Figure 4. Frequency of Algorithms (2020 – 2025)

Figure 4 shows the distribution of ML and XAI techniques used in malaria research from 2020 to 2025. Ensemble methods, such as Random Forest and XGBoost, are the dominant techniques in the field due to their ability to handle heterogeneous datasets, whereas deep learning is primarily used in high-dimensional imaging and geospatial analysis. Although SHAP and LIME are the dominant techniques in XAI, Causal AI has potential for use in the field but has been underrepresented. The trend shows a shift in the development of transparent ensemble methods to improve the performance of malaria diagnostic and forecasting tools.

D. Technology Readiness Level Assessment

The included studies were categorised using a simplified TRL framework.

- TRL 2-3 (Experimental): Studies relying on synthetic datasets or laboratory-based genomic modelling without external validation; such that [24],[15].
- TRL 4-5 (Validated in Research Setting): Models tested on retrospective regional datasets with cross-validation but without real-world deployment included studies [17], [25], [26]
- TRL 6-7 (Field-tested): Studies using real clinical or national surveillance data with high potential for public-health integration [10], [23], [36].
- TRL 8–9 (Operational Policy Deployment): No study demonstrated documented operational deployment within a national program at the time of publication

This analysis indicates that most XAI malaria models remain at pre-deployment maturity, highlighting a translational gap between research and implementation.

E. Discussion

This systematic review aims to identify the explainability needs in the context of climatic predictions and genomic knowledge. These two perspectives present a new research frontier that remains unexplored and underdeveloped. These findings are discussed collectively in the following sections:

RQ1: How does the comparative prediction capability of integrated multi-modal models compare with that of single modality approaches in the context of malaria incidence prediction?

The selected literature emphasizes single-modality modelling, thereby constraining the full scope of biological and epidemiological knowledge that may be obtained from such research. Of the twelve studies that were examined, eight were based on modelling with a single data stream [15], [17], [23]–[26].

1) *Strength of multi-modality:* Two studies within the corpus that effectively utilized diverse types of information had the strongest prediction results. A case example is the research by [16], which achieved 98% accuracy by combining clinical symptoms such as nausea and fever with environmental factors such as rainfall and temperature to forecast malaria risk in Kenya. Such an example supports the assertion that disease risk arises from multifaceted factors that interact.

2) Performance of Single-Modality: Single-modality models suffer from limited explanatory power. Climate-only models performed strongly for forecasting (such as the Transformer model's 80% AUROC [23]), demonstrating that weather variables are easy to measure and exhibit high temporal resolution for effective time-series analysis. Genomic models have proved highly effective for specialized classification of parasite origin, but their utility is restricted to classification rather than epidemiological forecasting [15].

The performances of these models indicate that the most significant gap is the lack of research on integrating genomic and climatic data. Such a framework is necessary to help understand how parasite evolution is influenced by environmental factors and clinical presentation and move the field towards holistic prediction. Field towards holistic prediction. Given projected climate change scenarios and the northward expansion of vector habitats, future malaria prediction systems must incorporate dynamic climate change modelling rather than static meteorological variables. Explainable AI frameworks capable of simulating climate-driven vector shifts and parasite adaptation will become critical under global warming trajectories. The absence of integrated climate–genomic models may limit preparedness for future transmission patterns in previously low-incidence regions.

RQ2: What are the ways in which the methods of "Explainable Artificial Intelligence" shed light on the role played by the combined data features in the outputs of complex malaria prediction models, and what influence does this have on the trust of stakeholders?

The discussion surrounding XAI has moved beyond simple feature ranking to include the generation of trust-enabling, clinically actionable interpretations. XAI was utilized in five studies (41.7%), with SHAP and LIME being the clear dominant techniques for interpretability [6], [16], [26], [27].

1) *LIME:* LIME (Local Interpretable Model-agnostic Explanation) creates a simple, local surrogate model around a single prediction to explain why the model made that specific decision [26], [36]. LIME was used in CNN-based models for enhanced malaria detection to interpret and highlight the specific regions in blood smear images that led the model to classify an image as positive, thereby improving trust among diagnosticians [8].

2) *SHAP:* A more consistent and global explanation for feature contribution is offered by SHAP (Shapley Additive Explanations) [25]. LIME and SHAP were applied to ensemble models (RF, XGBoost) to obtain explanations for malaria prediction and general malaria diagnosis [26], [36].

3) *Causal AI:* CAI helps establish a definitive cause-and-effect relationship between variables, as opposed to establishing a relationship through correlation [27]. The study by [10] presented the concept of CAI, which shows the evolution from establishing a relationship through correlation towards establishing the causal determinants of malaria outcomes. CAI, along with XGBoost and XAI, was employed as a tool towards establishing the critical determinants of the causes of malaria, which contribute to the mortality rates globally [27].

Despite their widespread use, SHAP and LIME have methodological limitations. SHAP, for instance, relies on feature independence, which may not hold in genomic SNP datasets, where features are often correlated. In addition, the stability of the LIME may be an issue, especially in the presence of small perturbations. The importance of features does not necessarily imply causality, which may lead to overinterpretation in public health.

Future XAI techniques in malaria modelling should also evaluate the robustness and fairness of explanations, particularly when models are deployed across heterogeneous demographic and geographic populations. Without stability testing, interpretability claims may not generalise across endemic regions.

RQ3: What is the performance of various algorithms of artificial intelligence and machine learning in terms of their accuracy and applicability on various data modalities?

Different AI and ML algorithms were compared and evaluated based on their characteristics and capabilities.

1) *Random Forest (RF):* The Random Forest model builds several decision trees during training, then combines the outputs of each decision tree as a prediction, which reduces the issue of overtraining[10], [38]. RF has been observed to be effective in predicting malaria incidence in Brazil during a given week, surpassing XGBoost, LSTM, etc., as it has the least Root Mean Squared Error in most clusters compared to other models [16].

2) XGBOOST: XGBoost (Extreme Gradient Boosting) is an optimized, high-performance implementation of gradient boosting that iteratively builds new decision trees to correct the errors of previous trees. Highly valued for speed and handling large datasets [10]. In detection, XGBoost achieved optimal overall performance for malaria detection using a validated synthetic clinical dataset, recording the highest AUC (0.956) [23]. In Regression for malaria incidence prediction using weather variables in Rwanda, XGBoost was marginally better than RF (R-squared 98.20% vs. 97.81%) [10].

3) *CNN:* A deep neural network specialized for processing grid-like data (e.g., images). It learns spatial feature hierarchies using convolutional layers [24].

Figure 5 compares the performance of ML models and AL algorithms, scaled by performance score.

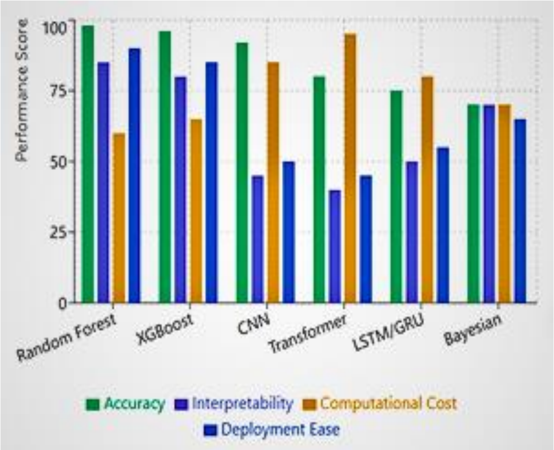

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Figure 5. Comparative performance of machine learning models used in malaria prediction

Figure 5 presents a comparative synthesis of the predictive performance and limitations of the most used machine learning models in malaria research. Ensemble models such as Random Forest and XGBoost have strong predictive power and interpretability. These models can thus be used for diagnostic prediction and incidence prediction. Deep learning models, such as Convolutional Neural Networks and Transformers, have high prediction potential when working with high-dimensional and time-dependent data, such as microscopy images and climate time series [39],[40]. However, the black-box nature of deep learning models necessitates additional models to improve interpretability.

RQ4: What actionable public health insights are available from XAI feature importance and causal inference to guide targeted malaria control interventions?

Four public health insights were derived from the XAI-generated feature importance and the causal analysis of the data set in the context of targeted malaria interventions:

A. Climate-Based Early Warning

XAI Finding: SHAP results showed rainfall was the primary predictor (35-45% variance) with 1-2 months of lag [16], [17].

Actionable insight: Utilize indoor residual sprays and insecticide-treated bed nets 4-6 weeks prior to peak outbreaks when rainfall exceeds 100 mm.

B. Cost-Effective Clinical Triage

Based on the findings that used SHAP, fever and low platelets were found to contribute 60-70% to the confidence level in predicting severe malaria [6].

Actionable insight: Utilize diagnostic protocols that emphasize clinical markers in urban or rural health centres, maintaining 95%+ accuracy while lowering lab expenditures [27].

C. Drug Resistance Surveillance

XAI Finding: ML models such as CNN's 'attention' feature identified geographic patterns of artemisinin resistance in Southeast Asia [15]. Actionable insight: Genomic surveillance should be prioritized in regions where XAI models indicate the highest levels of treatment intensity.

D. Intervention Synergy Quantification

XAI Finding: A combination of bed netting plus indoor spraying was shown by CAI to have a non-additive 35% case reduction compared with the 25% predicted from the individual effects [10]. Actionable insight: Use integrated intervention packages, not single-intervention approaches, to maximise health impact.

In Figure 6, a causal policy map shows how links climate variability, vector dynamics, genomic pressures, disease severity, and mortality risk

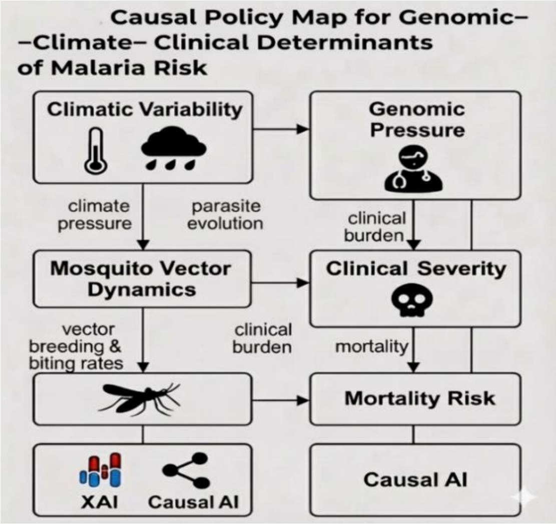

Figure 6. Causal policy map for genomic–climate–clinical determinants of malaria risk

Figure 6 map demonstrates the contribution of each domain to the overall risk of malaria. Climatic changes significantly affect vectors by altering breeding and biting rates. Such changes are also known to induce genomic alterations that lead to drug resistance. Explainable and causal AI tools can integrate all factors, provide risk indicators, and simulate scenarios that could have occurred.

E. Taxonomy of XAI by Data Modality and Definition of a Unified Integration Framework.

This review indicates that different XAI techniques are employed across modalities for malaria prediction. Thus, we propose a taxonomy for XAI methods by different data modalities.

- For climate models (mostly dealing with time series and spatio-temporal data), XAI methods like global feature attribution methods (SHAP values and permutation values) are used.
- For clinical models (mostly dealing with tabular patient data), XAI methods like SHAP values and LIME are used.
- For genomic models (mostly dealing with whole-genome sequencing, SNPs, and mutations in the parasite), XAI methods like deep learning models are used; however, domain-specific interpretability methods like mutation or feature visualization are not used.

A "unified multimodal framework" in this review is defined as: "A predictive modelling framework that integrates climatic, genomic, and clinical features simultaneously in a single architecture and uses XAI methods across all modalities to obtain coherent and policy-relevant findings." Unfortunately, the existing literature lacks a unified framework; instead, XAI methods are applied separately across modalities.

F. *Multi-Modal Explainable AI Conceptual Framework for Malaria Prediction*

Figure 7 presents a proposed framework that integrates climatic variables, genomic signatures based on parasite mutations, and clinical characteristics into a modelling pipeline using ensemble classifiers and deep learning to improve interpretability and support policymaking decisions.

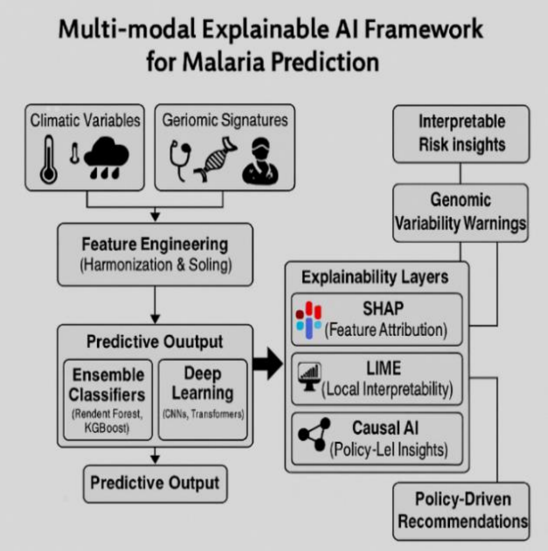

Figure 7. Multi-modal Explainable AI framework for malaria prediction

The conceptual model depicted in Figure 7 facilitates the integration of diverse data sources through feature engineering and normalization, followed by the application of advanced machine learning algorithms such as Random Forest, XGBoost, Convolutional Neural Networks (CNNs), and Transformers. Finally, the results from these models are aggregated into an interpretability model that incorporates SHAP, LIME, and Causal AI to bridge gaps in the literature. Overall, the model serves as a strategic roadmap for developing effective malaria prediction models that inform public health policymaking.

G. *Implications of the Study*

This review shows that XAI can enhance both the accuracy and interpretability of malaria prediction systems while simultaneously addressing the gap associated with black-box ML models

1) Practical implications: This review demonstrates that XAI is not merely beneficial but necessary for the scalable deployment of malaria prediction systems in real-world public health settings. By integrating SHAP, LIME, and Causal AI into ensemble and deep learning architectures, malaria prediction models can shift from opaque risk scoring to accountable decision-support tools. In low-resource environments, ensemble models such as Random Forest and XGBoost offer a practical balance between computational efficiency, predictive accuracy, and interpretability, making them suitable candidates for integration within national malaria surveillance systems. The proposed multimodal framework further provides a blueprint for early-warning systems that integrate climatic variability, shifts in parasite genomics, and clinical indicators to guide targeted intervention strategies.

2) *Theoretical implications:* The study advances computational epidemiology by reframing XAI as a foundational epistemological requirement rather than a post hoc interpretability add-on. By highlighting the structural limitations of single-modality models, it establishes multimodal data fusion as a theoretical imperative for modelling complex disease transmission systems. Furthermore, the integration of Causal Artificial Intelligence into malaria modelling represents a shift from correlational prediction toward intervention-oriented reasoning. This reorientation aligns AI-driven epidemiology with principles of AI governance, transparency, and policy accountability, particularly amid accelerating climate change and evolving parasite dynamics.

H. *Limitations of the study*

This review is subject to several methodological constraints that should be considered when interpreting the findings. First, the restriction to English-language publications may introduce regional publication bias, potentially underrepresenting studies conducted in francophone and lusophone malaria-endemic regions. Second, database selection (PubMed, IEEE Xplore, SpringerLink, and ScienceDirect) may have limited inclusion of regionally indexed journals, thereby influencing the geographic distribution of evidence.

Third, the 2020–2025-time restriction, although justified by the surge in model-agnostic XAI methods such as SHAP and LIME, may exclude earlier foundational machine learning work in malaria modelling. Fourth, substantial heterogeneity in datasets, validation protocols, and performance metrics constrained direct quantitative comparison across studies. The absence of standardised multimodal datasets further limits eneralizability and reproducibility across contexts.

Fifth, several included studies relied on synthetic or region-specific datasets, which may reduce external validity when extrapolating findings to broader epidemiological settings. Finally, publication bias toward high-performing models may inflate reported predictive accuracy, particularly where external validation was limited.

To mitigate these constraints, findings were interpreted in conjunction with structured risk-of-bias assessment, with greater analytical weight assigned to studies demonstrating robust validation, representative datasets, and substantive explainability implementation.

I. *Future works*

This review identifies five priority research directions to advance explainable, deployment-ready malaria prediction systems. First, the development of integrated multimodal datasets that combine climatic, genomic, and clinical variables, aligned across temporal and geographic scales, remains a critical infrastructural requirement. The absence of standardised benchmark datasets currently constrains reproducibility, comparability, and cross-model validation. Second, future systems must incorporate structural Causal Artificial Intelligence frameworks capable of simulating intervention scenarios and quantifying counterfactual policy outcomes. Without causal modelling, predictive systems remain descriptive rather than decision-enabling. Third, rigorous evaluation of the robustness and stability of explanations across geographic and demographic contexts is required. Interpretability claims must be tested for consistency to ensure equitable deployment across heterogeneous endemic regions. Fourth, domain-specific genomic interpretability methods should be developed to move beyond generic feature attribution toward mechanistic insights at the mutation level. Fifth, prospective validation within national malaria control programmes is essential to bridge the current translational gap between research prototypes and operational public health systems. Collectively, these priorities define a strategic transition from high-performing predictive models toward unified, causally informed, and policy-integrated XAI architectures that can support adaptive malaria control amid accelerating climate change and parasite evolutionary dynamics.

IV. CONCLUSION

This review demonstrates that Explainable Artificial Intelligence (XAI) is not merely an auxiliary feature of malaria prediction systems but a foundational requirement for trustworthy, deployable epidemiological modelling. Ensemble learning approaches, particularly Random Forest and XGBoost, provide strong interpretability and consistent performance in climate-driven and clinical forecasting contexts, whereas deep learning architectures excel in image-based and genomic analysis but require structured explainability overlays to address their inherent opacity.

Despite methodological advances, the review identifies three critical structural gaps: the limited use of Causal Artificial Intelligence for intervention simulation, the absence of fully unified multimodal frameworks that integrate climatic, genomic, and clinical determinants, and the lack of operational deployment in national malaria control programmes. These gaps constrain the transition from high-performing predictive models to actionable, policy-integrated decision support systems.

Given accelerating climate change and ongoing evolutionary dynamics of parasites, future malaria prediction systems must move beyond siloed modelling toward integrated, interpretable, and causally informed architectures capable of simulating the impact of interventions across heterogeneous ecological contexts. The strategic roadmap proposed in this review provides a foundation for advancing transparent, multimodal AI systems that bridge computational epidemiology and public health decision-making.

Developing unified, explainable, and deployment-ready malaria prediction frameworks is not simply a technical advancement; it is a necessary step toward resilient and adaptive disease control in an increasingly complex global health landscape.

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